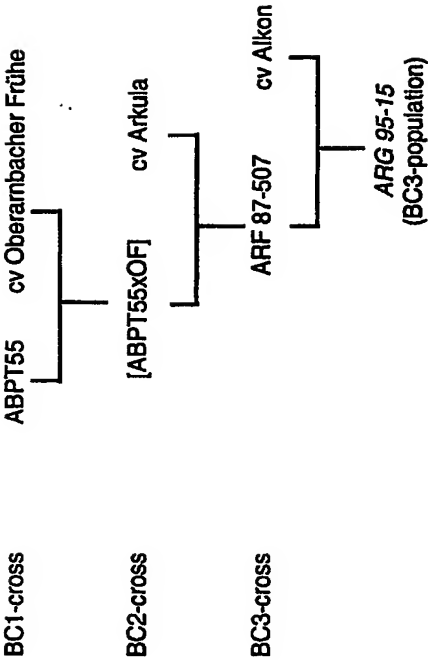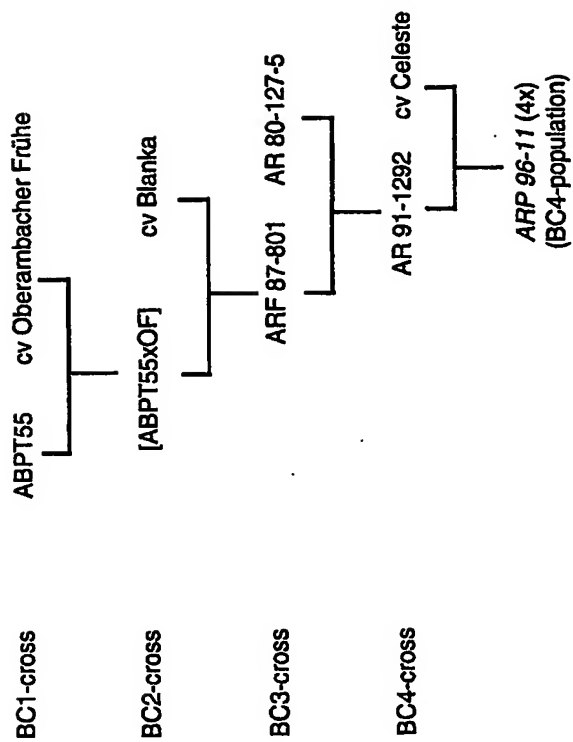Figure 1A

Figure 1B

Figure 1C
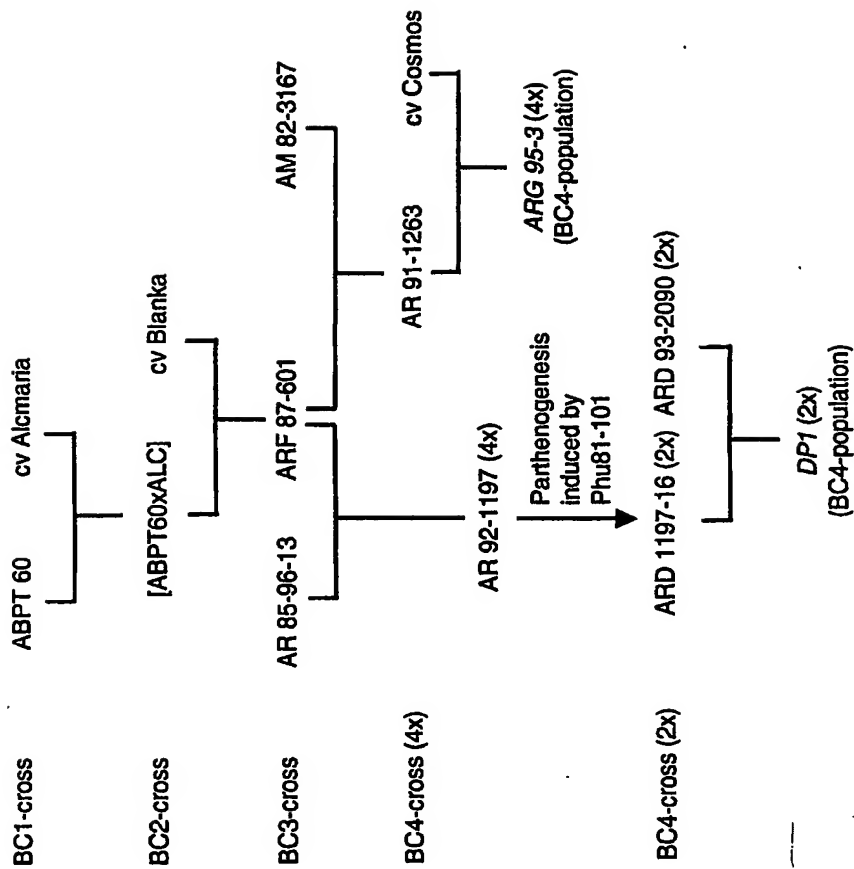
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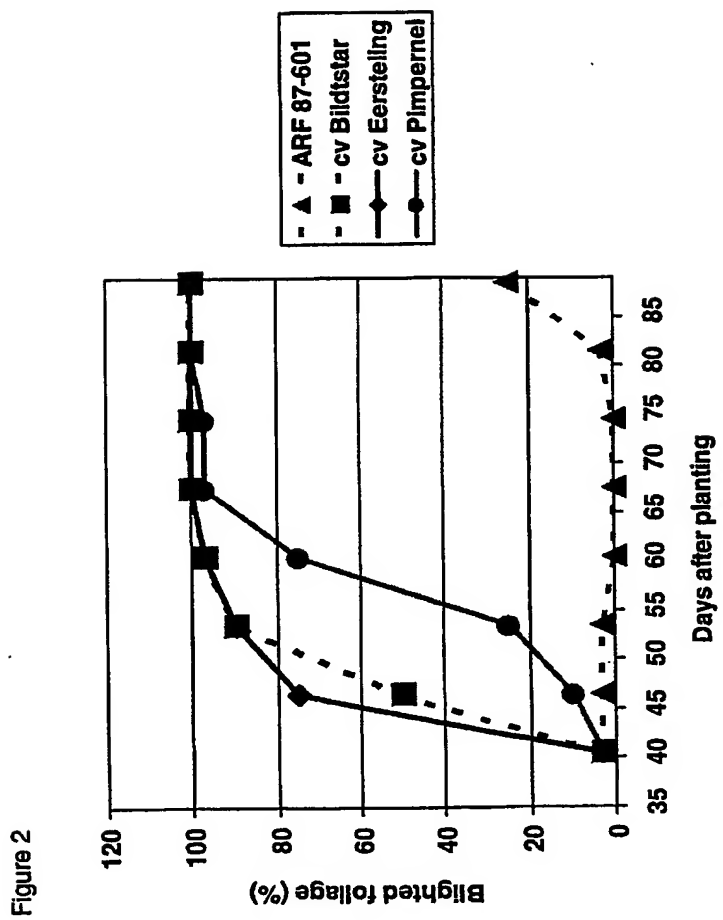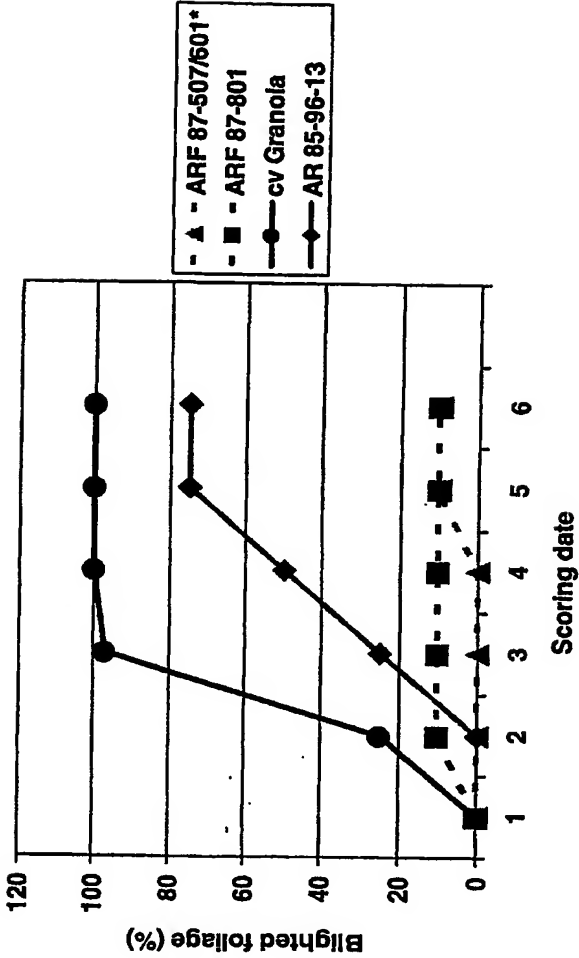
Figure 2

Figure 3

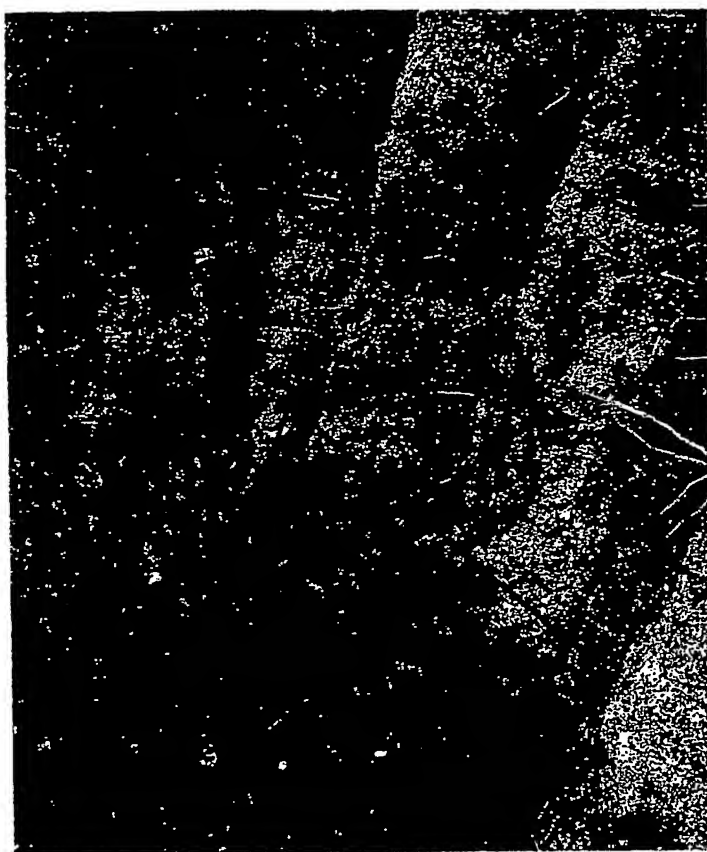* ARF 87-507 and ARF 87-601 had identical disease progress curves
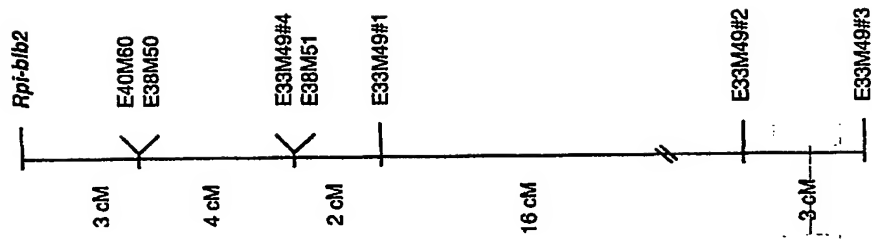
Figure 4

Figure 4 dia 3

Figure 4 dia 4

Figure 4 dia 5

Figure 4 dia 6
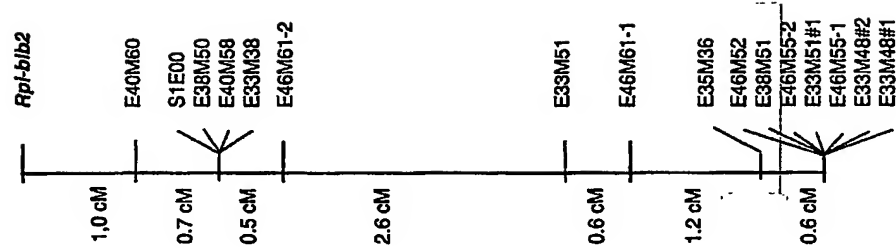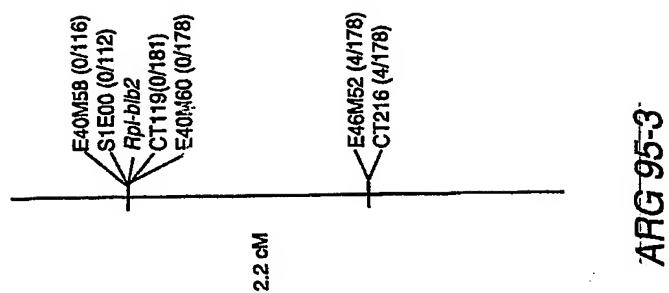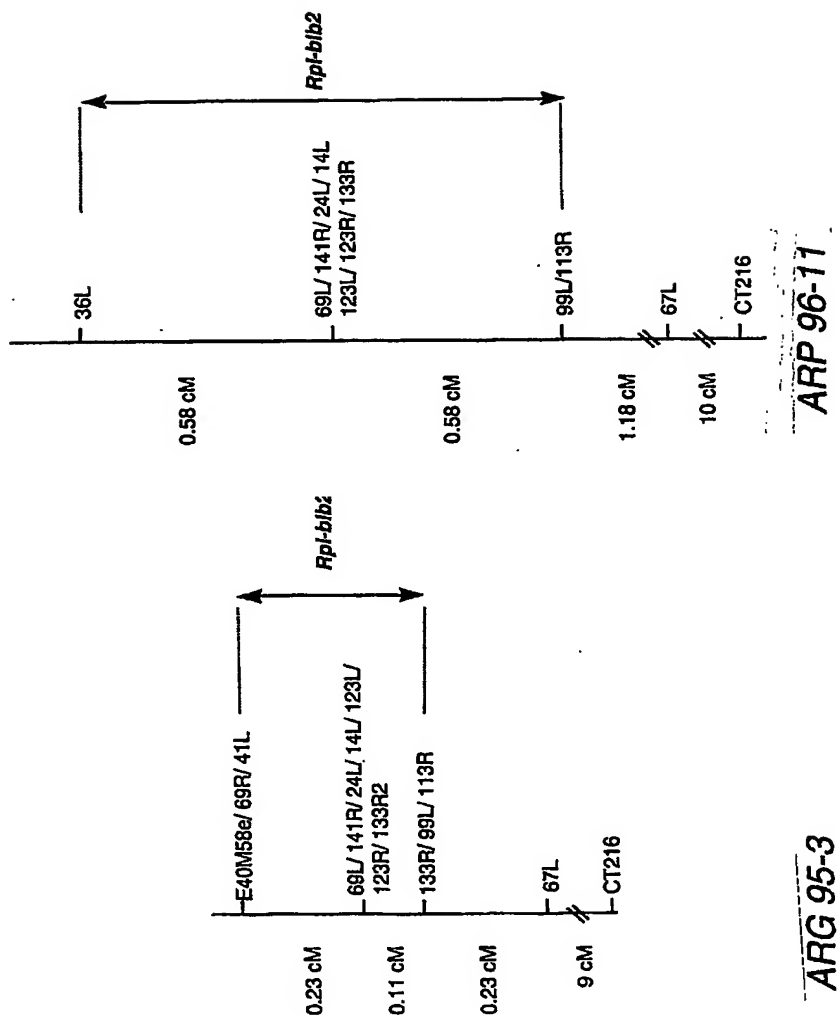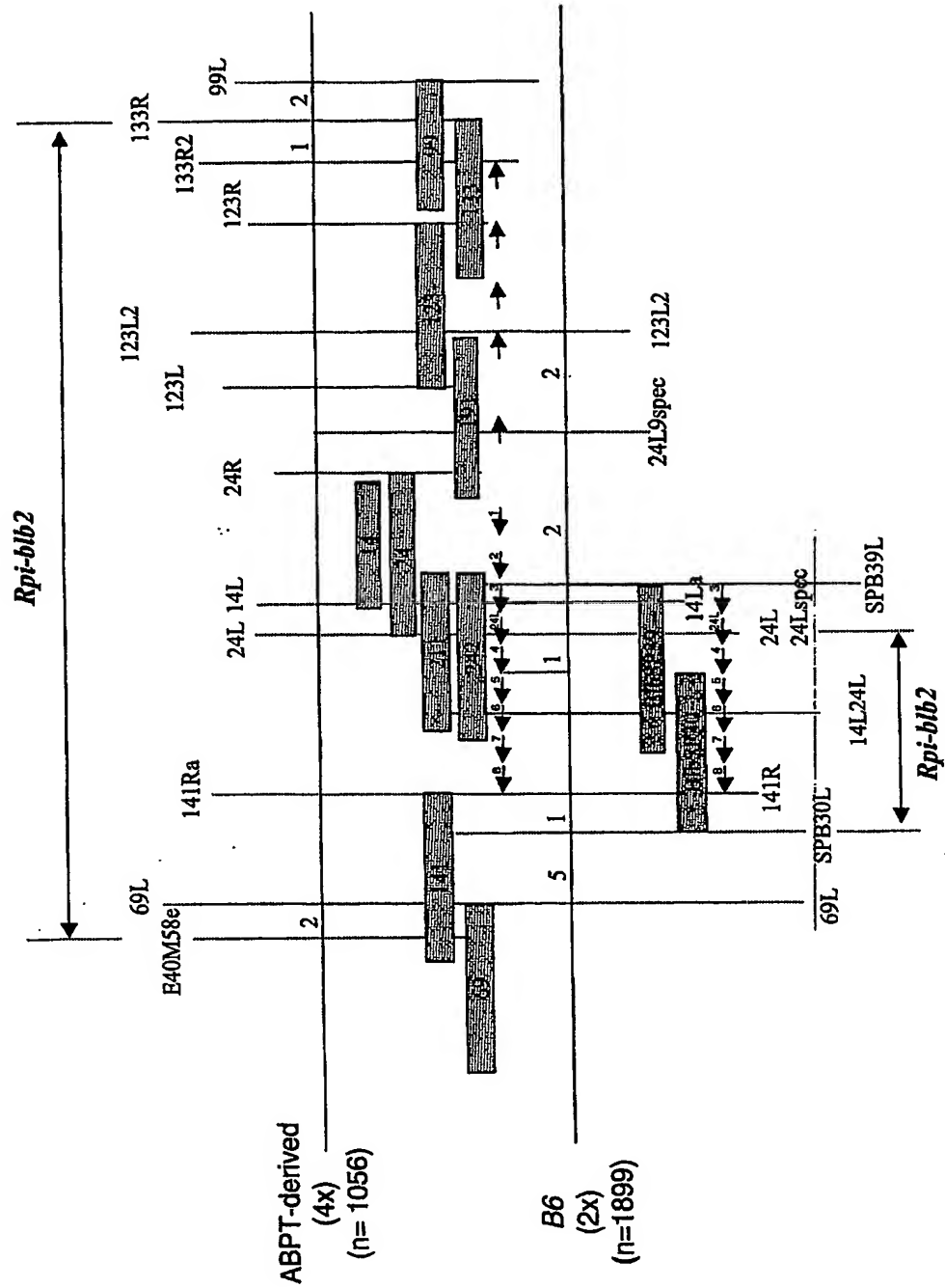
Figure 5

Figure 6

Figure 7

Figure 8

Figure 9
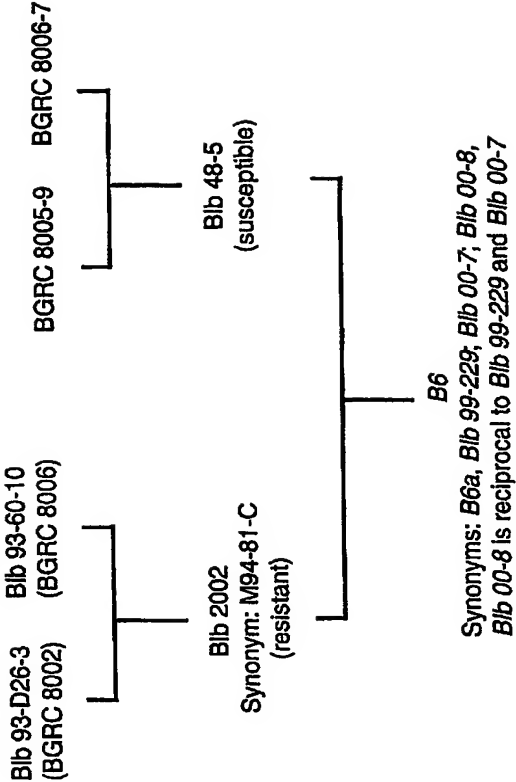
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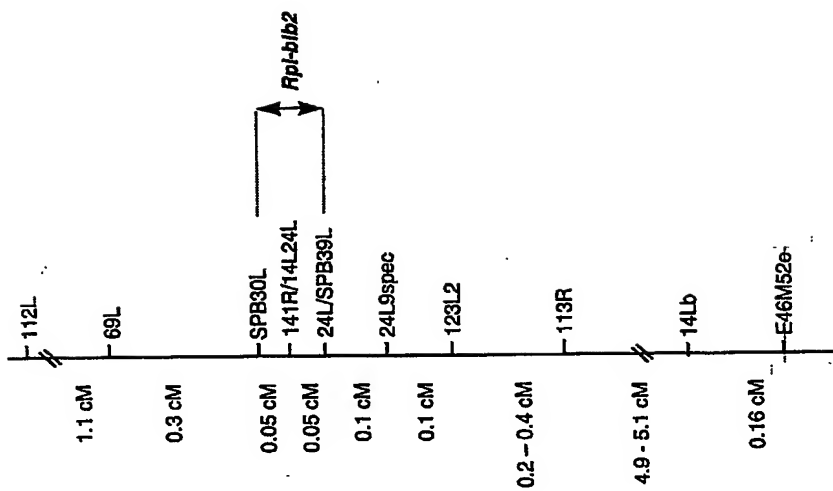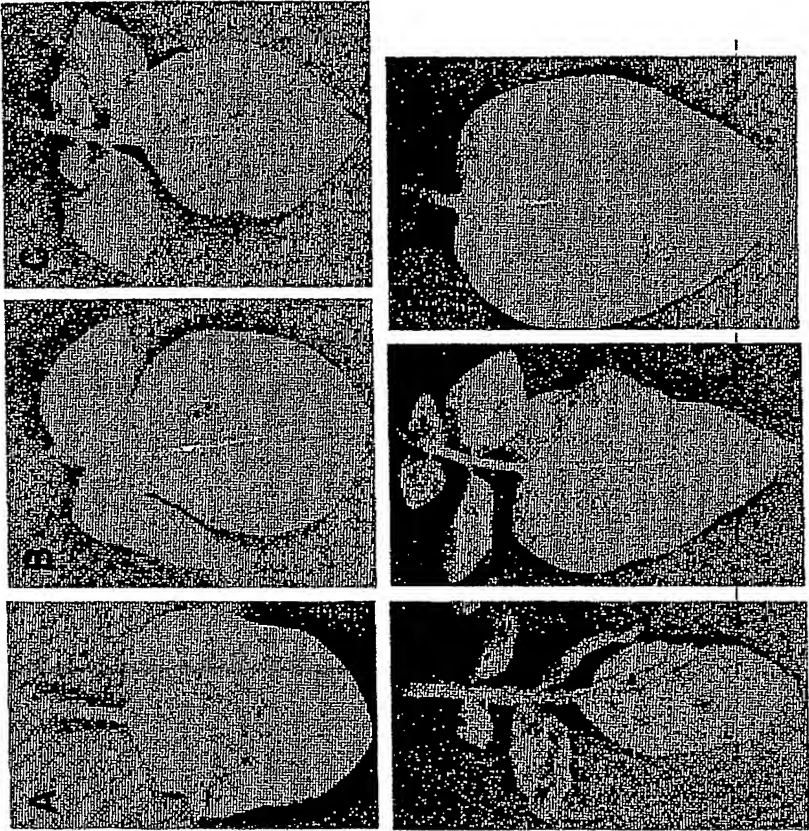
Figure 11

Figure 12
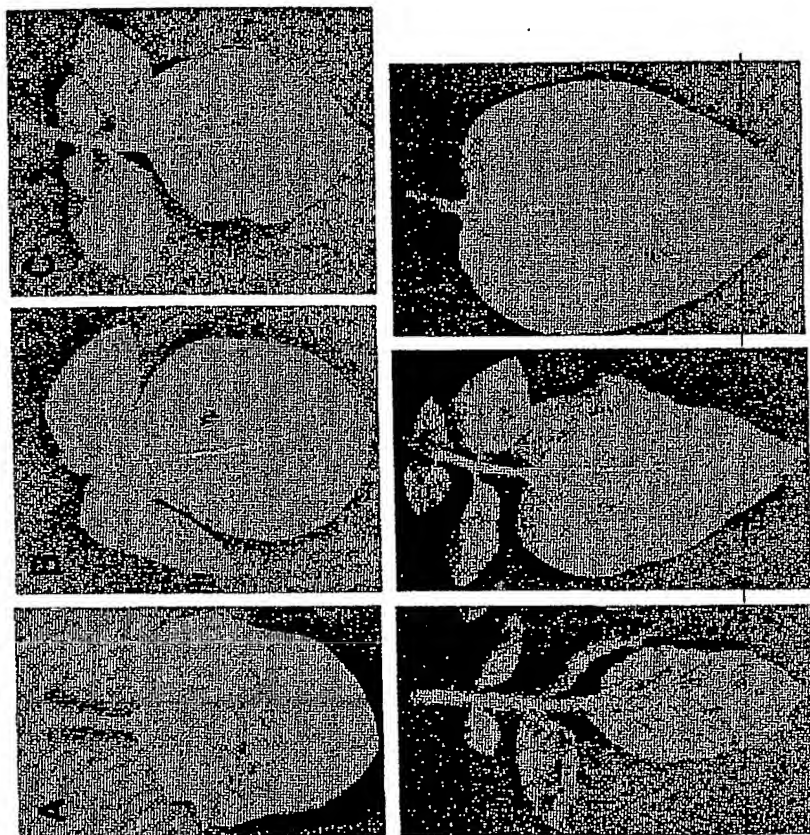
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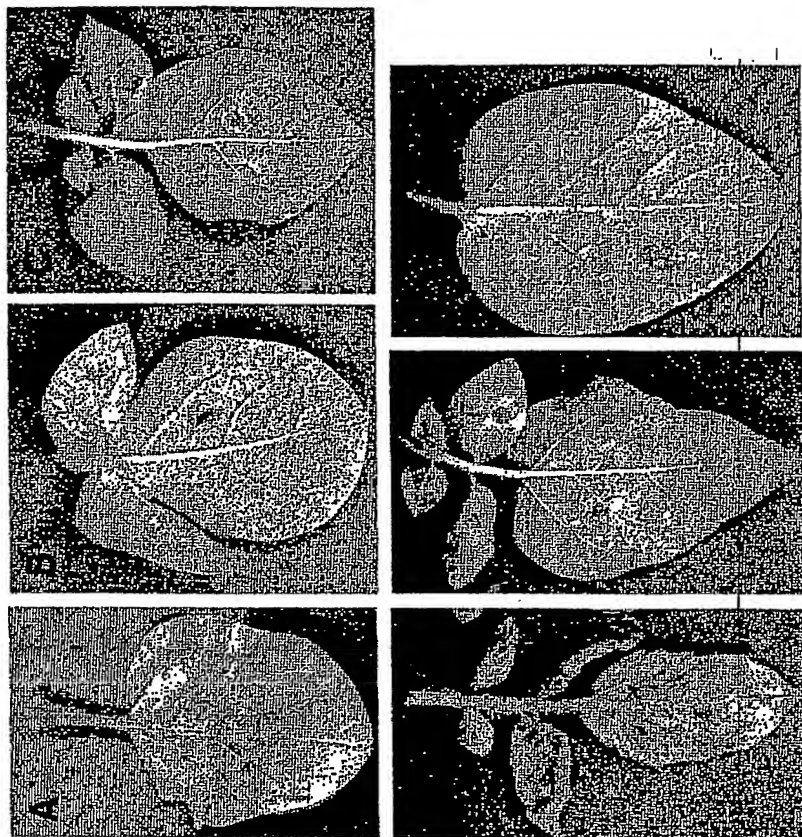
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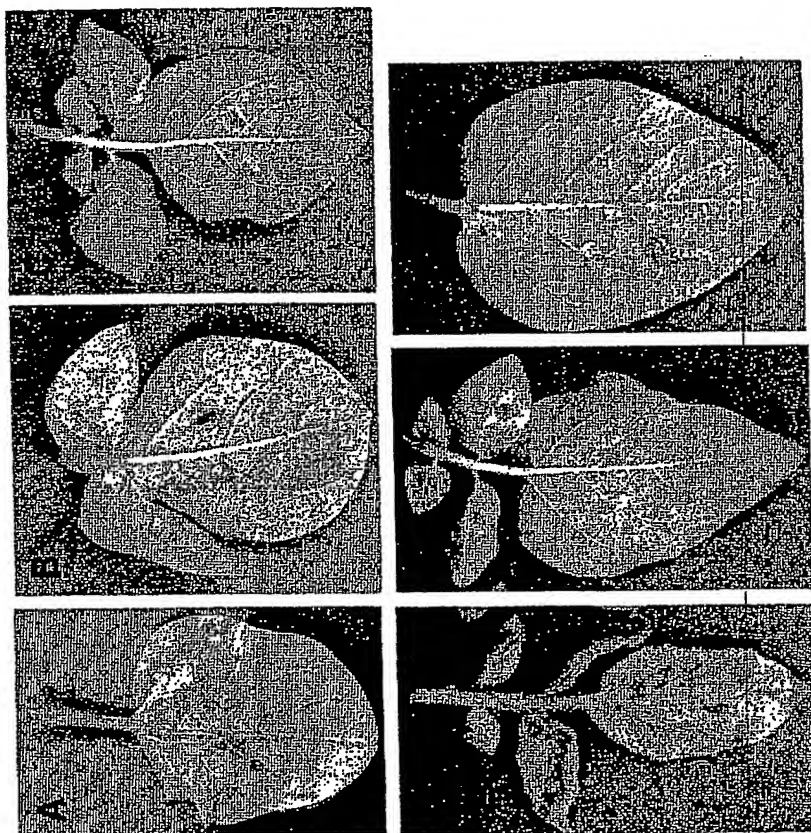
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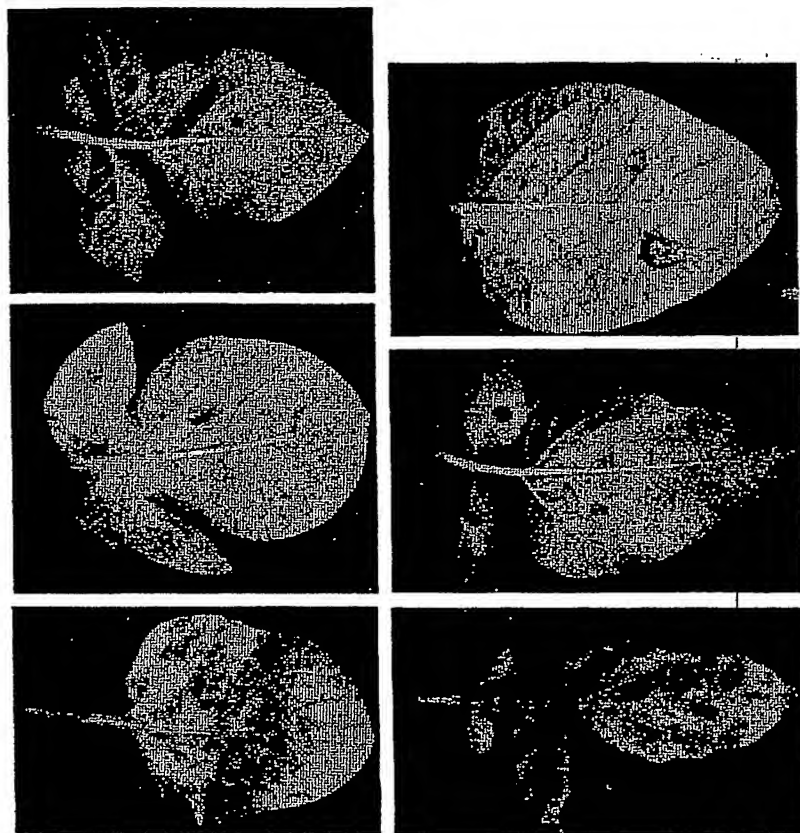
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Figure 13A

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Figure 13B

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Figure 13C

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Figure 13D

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PF 54801

42/51

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57
Mi1.2            I   VL     S  I    I   ---    N   L K QV KL    MA
57
Rpi-blb2  MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT
60

Mi1.1             C  F Q                 L    -------- F     TS
109
Mi1.2             Y  F Q   · N           SL   --------       TS
109
Rpi-blb2  YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR
120

Mi1.1        Y   I    D    Y   H  I          I              G
169
Mi1.2        Y   I    D    Y   H  I                        L G
169
Rpi-blb2  S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI
179

Mi1.1           P     D  H  D  T    R      E    R SR
229
Mi1.2           P        H     T    R      EH   R SR  Q T
229 Rpi-blb2
     KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239

Mi1.1        V   I   TN     A V L  Q   .          P    V     S
289
Mi1.2            TN      A V            I Q     L   P S L
289
Rpi-blb2  PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR
299

Mi1.1           L     -         D  GV              EP N   GNNQ
348
Mi1.2           L     -         H  GT                 N   GNNQ
348
Rpi-blb2  NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE
359

Mi1.1         DL      K      AL    C          HI  N
408
Mi1.2         DL      K      A N   C          HM  N
408
Rpi-blb2  TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS
419

Mi1.1         E E    Q  K      VD-A         A                ·
467
Mi1.2     S   E E  SQE         GDAA       I A
468
Rpi-blb2  IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL
478
          -------------------

Mi1.1          I  IK     I A D   P D   .          R        T   E
527
Mi1.2          I  IK   . I A D   P D              R        I   E
528
Rpi-blb2  HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE
538

Mi1.1             S      T   S               R          GC
587
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PF 54801

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Mi1.2                          T      S                    R              G  D
588
Rpi-blb2  TNLILRKLTSGPADLDVISIIgmpglgkttlaYKVYNDKSVSSHFDLRAWCTVDQVYDEK
598

Mi1.1        NT  S      D                  .                     T          ESK
647
Mi1.2         T  S   G  D  N                               T  L          EAK
648
Rpi-blb2  KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKrylivlddvwDTNTWDELTRPFPDGM
658

Mi1.1               E       N      D    PD
707
Mi1.2               E       N      D    PD        D  T
708
Rpi-blb2  KGSRIILTTREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCPDELLDVGKEI
718

Mi1.1            A      V         R      QSS S      NS          L        H
767
Mi1.2            A      V         R      QSS S      NS          L        H
768
Rpi-blb2  AENCKglplvvdliagIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH
778

Mi1.1            F    TSL  Y  NVYF A     G    E  N  M        M     Y
827
Mi1.2         H  W    TPL  YLFTVYL A          E  GI        M
828
Rpi-blb2  lkpcllyfasAPKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF
838

Mi1.1        YALNF I            N  F  Q  R              T  C  EE -
886
Mi1.2        ILNF I             N  F     R              T     EE
888
Rpi-blb2  NEIGDYPTCQlhdlvhdFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF
898                                                                 ──────
                                                                    ──►LRR
Mi1.1      M  D            R  I  Q    SV  A           ┌─────┐HT
946                                                   │V  D │
Mi1.2      M  D            R     Q    SV  A        I  │V  D │ P  L    N
948                                                   └─────┘
Rpi-blb2  VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE
958       ──────────────   ─────────────          ────────────
              1                 2                         3
Mi1.1          D  Q  Y               S    STNR   V      L      R  SVD
1006
Mi1.2          R  R Q  Y  F          S    S  G  I V      L      R  SVG
1008
Rpi-blb2  ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA
1018             ─────────────          ──────────          ──────────
                  4                       5                        6
Mi1.1                     RI T  LI  S   KN      F       L S E
1066
Mi1.2             K       RI    LI  S   MN      F         Q E
1068
Rpi-blb2  CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY
1078               ──────────       ─────────             ─────────
                   7                  8                     9
Mi1.1      H  SE        T  S  G  KS         V  T        N  I  W  R
1126
Mi1.2      H     C      T  C  G  KS    HC   VVT         N  E  L  YD
1128
```

PF 54801

```
Rpi-blb2    STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT
1138
                                      10                                 11
Mi1.1                 P      S   H                    F NFN   SI
1186
Mi1.2                 P    N S   D   Q       .        F N RLLT
1188
Rpi-blb2    SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP
1198
                                      12                        13
Mi1.1       N      K RG   K         P          S KI K      D
1246
Mi1.2       N      K QE GK          P          F KI K      D       K        ND
1248
Rpi-blb2    TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL
1258
                      14                              15
Mi1.1            N        1255
Mi1.2            N        1257
Rpi-blb2    GQKDIPLFK 1267
```

Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mil.1   3768 bp
Sequence 2: Mil.2   3774 bp
Sequence 3: Rpi-blb2   3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2   Score:68908
Group 2: Sequences: 3   Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Figure 17: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: Mi1.1         1255 aa
Sequence 2: Mi1.2         1257 aa
Sequence 3: Rpi-blb2      1267 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree        file created:    [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14322840.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:    2          Score:25939
Group 2: Sequences:    3          Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14322840.aln]


CLUSTAL W (1.82) multiple sequence alignment


Mi1.1        MEKRKDNEEANNSLVLFSALSKDIADVLVELE---NEENQKALDKDQVEKIKLKMAFICT 57
```

```
Mi1.2     MEKRKDIEEANNSLVLFESALSKDIANVLIFLE---NEENQKALDKDQVEKLKLKMAFICT  57
Rpi-blb2  MEKRKDNEEANNSLESFSALRKDAANVLDFELERLKNEEDQKAVDVDLIESLKLTFICT   60
          ***** ** ******** ***** ** *:** ***  ***.***:.*:***

Mi1.1     YVQLSCSDFEQFEDIMTRKRQEVENLLQPLLDDD-------VFTSLTSNMDDCISLYHR  109
Mi1.2     YVQLSYSDFEQFEDIMTRNRQEVENLLQSLLDDD-------VLTSLTSNMDDCISLYHR  109
Rpi-blb2  YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR 120
          *****  ***  :****** ******.:*****       .:***** :**********

Mi1.1     SYKSDAIMMDEQLDEFLLINLYHLSKHHAEKIFPGVTQYEVLQNICGNIRDFHGLIVNGCI 169
Mi1.2     SYKSDAIMMDEQLDEFLLINLYHLSKHHAEKIFPGVTQYEVLQNVCGNIRDFHGLILNGCI 169
Rpi-blb2  S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI  179
          * **** ******  *****  *****:***:************:*************:* **

Mi1.1     KHEMVENVLPLFQLMADRVGHFLWDDQTDEDSRLSELDEDEQNDRDSRLFKLAHLLLKIV  229
Mi1.2     KHEMVENVLPLFQLMAERVGHFLWEDQTDEDSRLSELDEDEHNDRDSRLFQLTHLLLKIV  229
Rpi-blb2  KHEMVENVLSLFQLMAERVGRFLWEDQAQEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV  239 .
          ********* *****:***.***:** :**** *:******.::**:*.:**:* ********

Mi1.1     PVELEVIHICYTNLKASTSAEVGLFIKQLLETSPDILREYLIPLQEHMVTVITPSTSGAR  289
Mi1.2     PTELEVMHICYTNLKASTSAEVGRFIKKLLETSPDILREYIIQLQEHMLTVIPPSTLGAR  289
Rpi-blb2  PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR  299
          * *****:****  .:.*****:.  *****:**********:*:****:** .* *** 

Mi1.1     NIHVMMEFLLILSDMP-KDFIHHDKLFDLLDRVGVLTREVSTLVRDLEEEPRNKEGNNQ  348
Mi1.2     NIHVMMEFLLILSDMP-KDFIHHDKLFDLLAHVGTLTREVSTLVRDLEEKLRNKEGNNQ  348
Rpi-blb2  NIHVMMEFLLILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE  359
          *************** *************:*  :  .**********:*  .::

Mi1.1     TNCATLDLLENIELLKKDLKHVYLKALDSSQCCFPMSDGPLEMHLLHIHLNDLLDSNAYS 408
Mi1.2     TNCATLDLLENIELLKKDLKHVYLKAPNSSQCCFPMSDGPLFMHLLHMHLNDLLDSNAYS 408
```

```
Rpi-blb2   TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS  419
           ************.:.***********.  :.*** **.:.*.:************

Mi1.1      IALIKEEIELVKQDLKFIRSFEVD-AEQGLYKDLWARVLDVAYEAKDVIDSIIVRDNGLL  467
Mi1.2      ISLIKEEIELVSQELEFIRSFEFGDAAEQGLYKDIWARVLDVAYEAKDVIDSIIVRDNGLL 468
Rpi-blb2   IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL  478
           *.:*****:*  **..::*.:.******* :  ************:***************

Mi1.1      HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKITVGFEEE  527
Mi1.2      HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKIIVGFEEE  528
Rpi-blb2   HLIFSLPITRKKMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE   538
           ********* **.:. ****.:.** *.:.******************** *** ** **

Mi1.1      TNLILRKLTSGSADLDVISITGMPGSGKTTLAYKVYNDKSVSSREDLRAWCTVDQGCDEK  587
Mi1.2      TNLILRKLTSGPADLDVISITGMPGSGKTTLAYKVYNDKSVSRHFDLRAWCTVDQGYDDK  588
Rpi-blb2   TNLILRKLTSGPADLDVISIIGMPGLGKTTLAYKVYNDKSVSSHFDLRAWCTVDQVYDEK  598
           ********** *.******** ***. ************** :.********** *.:.*

Mi1.1      KLLNTIFSQVSDSDSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTWDELTRPFPESK  647
Mi1.2      KLLDTIFSQVSGSDSNLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTLDELTRPFPEAK  648
Rpi-blb2   KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTNTWDELTRPFPDGM  658
           ***:.**.***.*.*.************************************.* ****

Mi1.1      KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLEKRAFGNESCPDELLDVGKEI  707
Mi1.2      KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLDKRTFGNESCPDELLDVGKEI  708
Rpi-blb2   KGSRIILTTREKKVALHGKLYTDPLNIRLLRSEESWELLEKRAFGNESCPDELLDVGKEI  718
           ************:.******* ****:.:.****.:.*****:.**.:.*******

Mi1.1      AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH  767
Mi1.2      AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH  768
Rpi-blb2   AENCKGLPLVVDLIAGIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH  778
           **********.****:.*******.:.******. *.:.****.:.*********:.*****
```

```
Mi1.1      LKPCLLYFASFPKDTSLTIYELNVYFGAEGFVGKTEMNSMEEVVKIYMDDLIYSSLVICF  827
Mi1.2      LKPCLLHEASWPKDTPLTIYLFTVYLGAEGFVGKTEMKGIEVVKIYMDDLISSSLVICF   828
Rpi-blb2   LKPCLLYFASAPKDWVTTIHELKLIIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICE 838
           ******* .  *** *** ** **  : *:  ************:.:*****:*******

Mi1.1      NEIGYALNFQIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPRQITIDCDEEE-HFGLNF  886
Mi1.2      NEIGDILNFQIHDLVHDFCLIKARKENLFDRIRSSAPSDLLPRQITIDYDEEEEHFGLNF  888
Rpi-blb2   NEIGDYPTCQLHDLVHDFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF  898
           ****      *:***************:.* **:**********:**: :*.   ******

Mi1.1      VMFDSNKKRHSGKHLYSLRIIGDQLDDSVSDAFHLRHLRLLRVLDLHTSFIMVKDSLLNE  946
Mi1.2      VMFDSNKKRHSGKHLYSLRINGDQLDDSVSDAFHLRHLRLRLRVLDLEPSLIMVNDSLLNE 948
Rpi-blb2   VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE  958
           *:*.************** * **:**  **:*********:* * * ..  *** ******

Mi1.1      ICMLNHLRYLSIDTQVKYLPLSFSNLWNLESLFVSTNRSILVLLPRILDLVKLRVLSVDA  1006
Mi1.2      ICMLNHLRYLRIRTQVKYLPFSFSNLWNLESLFVSNKGSILVLLPRILDLVKLRVLSVGA  1008
Rpi-blb2   ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA  1018
           **********.* *:** **:**********:***.:. ::*:**** *****:**:  *

Mi1.1      CSFFDMDADESILIAEDTKLENLRILTELLISYSKDTKNIFKRFPNLQLLSFELKESWDY  1066
Mi1.2      CSFFDMDADESILIAKDTKLENLRILGELLISYSKDTMNIFKRFPNLQVLQFELKESWDY  1068
Rpi-blb2   CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY  1078
           ***************.:******   :**::** ***.:***** *****: *:*******

Mi1.1      STEQHWFSELDFLTELETLSVGFKSSNTNDSGGSSVATNRPWDFHEFPSNLKILWLREFPLT 1126
Mi1.2      STEQHWFPKLDCLTELETLCVGFKSSNTNHCGSSVVTNRPWDFHEFPSNLKELLLYDFPLT  1128
Rpi-blb2   STEQYWFPKLDFLTELELTVDFFERSNTNDSGGSSAAINRPWDFHEFPSSLKRLQLHEFPLT 1138
           ****:**  :*:*****  .* *  .:*   :***:.  ***********.:* : : ****
```

```
Mi1.1      SDSLSTIARLPNLEELSLYHTIIHGEEWNMGEEDTFENLKFLNENQVSISKWEVGEESFP 1186
Mi1.2      SDSLSTIARLPNLENLSLYDTIIQGEEWNMGEEDTFENLKFLNLRLLTLSKWEVGEESFP 1188
Rpi-blb2   SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP 1198
           ********** *** *** :******************** ** ::  *.:**********

Mi1.1      NLEKLKLRGCHKLEEIPPSFGDIYSLKSIKIVKSPQLEDSALKIKEYAEDMRGGDELQIL 1246
Mi1.2      NLEKLKLQECGKLEEIPPSFGDIYSLKFIKIVKSPQLEDSALKIKKYAEDMRGGNDLQIL 1248
Rpi-blb2   TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL 1258
           .*****.*  :******.*********** * *::*.****** **********:.****

Mi1.1      GQKNIPLFK 1255
Mi1.2      GQKNIPLFK 1257
Rpi-blb2   GQKDIPLFK 1267
           ***:*****
```

Figure 18